

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/521,162
Source: PCT/10
Date Processed by STIC: 1/25/05

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PCT

RAW SEQUENCE LISTING

DATE: 01/25/2005

PATENT APPLICATION: US/10/521,162

TIME: 10:02:45

Input Set : A:\FC-11-PCT.ST25.txt

Output Set: N:\CRF4\01252005\J521162.raw

3 <110> APPLICANT: Brandt, Kevin S.
 5 <120> TITLE OF INVENTION: FLEA AND TICK OCTOPAMINE RECEPTOR NUCLEIC ACID MOLECULES,
 6 PROTEINS AND USES THEREOF
 8 <130> FILE REFERENCE: FC-11-PCT
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/521,162
 C--> 11 <141> CURRENT FILING DATE: 2005-01-13
 13 <150> PRIOR APPLICATION NUMBER: 60/319,402
 14 <151> PRIOR FILING DATE: 2003-07-17
 16 <150> PRIOR APPLICATION NUMBER: 60/426,601
 17 <151> PRIOR FILING DATE: 2003-11-15
 19 <160> NUMBER OF SEQ ID NOS: 50
 21 <170> SOFTWARE: PatentIn version 3.2
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 111
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Ctenocephalides felis
 28 <400> SEQUENCE: 1
 29 gatatgtcgc tgtcaccagg ccagttgctt atccgagcat catgtctacg aaagggctaa 60
 31 gggactcata gccgggcttt ggggtcttag tttgtgatc tgcttccac c 111
 34 <210> SEQ ID NO: 2
 35 <211> LENGTH: 111
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Ctenocephalides felis
 39 <400> SEQUENCE: 2
 40 ggtgggaagc agatcacaaa actaagaacc caaagcccgg ctatgagtc cttagccctt 60
 42 tcgtagacat gatgctcgga taagcaactg gcttgggtgac agcgacatat c 111
 45 <210> SEQ ID NO: 3
 46 <211> LENGTH: 2061
 47 <212> TYPE: DNA
 48 <213> ORGANISM: Ctenocephalides felis
 51 <220> FEATURE:
 52 <221> NAME/KEY: CDS
 53 <222> LOCATION: (3)..(1679)
 55 <220> FEATURE:
 56 <221> NAME/KEY: misc_feature
 57 <222> LOCATION: (192)..(192)
 58 <223> OTHER INFORMATION: The "Xaa" at location 192 = Ala or Thr
 60 <220> FEATURE:
 61 <221> NAME/KEY: misc_feature
 62 <222> LOCATION: (193)..(193)
 63 <223> OTHER INFORMATION: The "Xaa" at location 193 = Asn or Tyr
 65 <400> SEQUENCE: 3
 66 at aga tat gtc gct gtc acc agg cca gtt gct tat ccg agc atc atg 47

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67   Arg Tyr Val Ala Val Thr Arg Pro Val Ala Tyr Pro Ser Ile Met
68     1             5             10             15
70 tct acg aaa agg gct aag gga ctc ata gcc ggg ctt tgg gtt ctt agt      95
71 Ser Thr Lys Arg Ala Lys Gly Leu Ile Ala Gly Leu Trp Val Leu Ser
72           20             25             30
74 ttt gtg ata tgc ttt cca cct tta gtc gga tgg aaa gat aaa aag gaa      143
75 Phe Val Ile Cys Phe Pro Pro Leu Val Gly Trp Lys Asp Lys Lys Glu
76           35             40             45
78 tcc gag gat ctg ata gac ata tct tca tgt cct tgg acg tgc gag ttg      191
79 Ser Glu Asp Leu Ile Asp Ile Ser Ser Cys Pro Trp Thr Cys Glu Leu
80           50             55             60
82 acg aac gat gca gga tat gtg gtg tat tct gct ctc gga tca ttc tac      239
83 Thr Asn Asp Ala Gly Tyr Val Val Tyr Ser Ala Leu Gly Ser Phe Tyr
84           65             70             75
86 att cct atg ttt gtc atg tta ttt ttc tac tgg agg ata tat aga gca      287
87 Ile Pro Met Phe Val Met Leu Phe Phe Tyr Trp Arg Ile Tyr Arg Ala
88 80           85             90             95
90 gct gtc agg aca acc aga gct atc aac caa gga ttc agg act aca aaa      335
91 Ala Val Arg Thr Thr Arg Ala Ile Asn Gln Gly Phe Arg Thr Thr Lys
92           100            105            110
94 ggt tgc cgt ggt ata gga cga ttt gac gaa caa cgc cta act tta agg      383
95 Gly Ser Arg Gly Ile Gly Arg Phe Asp Glu Gln Arg Leu Thr Leu Arg
96           115            120            125
98 att cat aga gga cgg ggt ggt tct gaa aat aga aga tgt cat cat cat      431
99 Ile His Arg Gly Arg Gly Gly Ser Glu Asn Arg Arg Cys His His His
100          130            135            140
102 tct tcc att aaa agt aat gct tca ggg aga atg tct aca tct aca tct      479
103 Ser Ser Ile Lys Ser Asn Ala Ser Gly Arg Met Ser Thr Ser Thr Ser
104          145            150            155
106 atg agg aat tgt tct cct caa cat agt tca cca cgt agt gca agt acc      527
107 Met Arg Asn Cys Ser Pro Gln His Ser Ser Pro Arg Ser Ala Ser Thr
108 160           165           170           175
110 agc tta gga agt act cac gaa tca cct gaa aaa tca tct ata tca agg      575
111 Ser Leu Gly Ser Thr His Glu Ser Pro Glu Lys Ser Ser Ile Ser Arg
112          180           185           190
114 rcc wac acc tgg gtt ttg cat cat gcg acc aat aat tcc aat tca gga      623
W--> 115 Xaa Xaa Thr Trp Val Leu His His Ala Thr Asn Asn Ser Asn Ser Gly
116          195           200           205
118 gct tgt aac caa gtc gtc att gcc aat aat aca agt caa agt gca cca      671
119 Ala Cys Asn Gln Val Val Ile Ala Asn Asn Thr Ser Gln Ser Ala Pro
120          210           215           220
122 aac aat aat cag tta aat agt acc cag cct gar gtc act gtg aca aaa      719
123 Asn Asn Asn Gln Leu Asn Ser Thr Gln Pro Glu Val Thr Val Thr Lys
124          225           230           235
126 agt agt cga aga tct tcg aaa tca tat aag agc ttt aaa aag gaa aga      767
127 Ser Ser Arg Arg Ser Ser Lys Ser Tyr Lys Ser Phe Lys Lys Glu Arg
128 240           245           250           255
130 gtt caa att tcg gtg cag tat cca agt gca gaa aga ctt gat gaa ttg      815
131 Val Gln Ile Ser Val Gln Tyr Pro Ser Ala Glu Arg Leu Asp Glu Leu

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132		260		265		270	
134	gaa ggt gaa tta gaa ggt gat gct	aca aac aac atg tac acc gtc cac	863				
135	Glu Gly Glu Leu Glu Gly Asp Ala Thr Asn Asn Met Tyr Thr Val His						
136		275 280 285					
138	tac tct gtg tcc aat ggt aac agc ttg tca aat cat tcg ttg atg cca	911					
139	Tyr Ser Val Ser Asn Gly Asn Ser Leu Ser Asn His Ser Leu Met Pro						
140		290 295 300					
142	gag cag caa ata gtc gat tct tcg agc caa caa cag acc att aga gca	959					
143	Glu Gln Gln Ile Val Asp Ser Ser Ser Gln Gln Gln Thr Ile Arg Ala						
144		305 310 315					
146	aca aca aca att aac ggt gat cag caa tta aat tcg ggt tcc atc tat	1007					
147	Thr Thr Thr Ile Asn Gly Asp Gln Gln Leu Asn Ser Gly Ser Ile Tyr						
148	320 325 330 335						
150	cgg cca cag gat aat cat cat ctc cga gtt acg tcg caa aga ttg gca	1055					
151	Arg Pro Gln Asp Asn His His Leu Arg Val Thr Ser Gln Arg Leu Ala						
152		340 345 350					
154	ccg tcg cct aca ctg tcg aag gga atg cat agg cga tcc agc agc tgc	1103					
155	Pro Ser Pro Thr Leu Ser Lys Gly Met His Arg Arg Ser Ser Ser Cys						
156		355 360 365					
158	gat agt aga gat ttg gct ggg ttt caa tta tgc gaa agt tca agt cca	1151					
159	Asp Ser Arg Asp Leu Ala Gly Phe Gln Leu Cys Glu Ser Ser Ser Pro						
160		370 375 380					
162	agt cca aca aga agg ata atg tct gga agt ctt tat cgt gat gat agc	1199					
163	Ser Pro Thr Arg Arg Ile Met Ser Gly Ser Leu Tyr Arg Asp Asp Ser						
164		385 390 395					
166	gag tta ggt tcg act tcc aaa ctg cag cag caa aat aga aaa atg ggc	1247					
167	Glu Leu Gly Ser Thr Ser Lys Leu Gln Gln Gln Asn Arg Lys Met Gly						
168	400 405 410 415						
170	aaa cgt aat ata aaa gct cag gtg aaa cgg ttt cga atg gag acg aaa	1295					
171	Lys Arg Asn Ile Lys Ala Gln Val Lys Arg Phe Arg Met Glu Thr Lys						
172		420 425 430					
174	gct gcc aaa aca ctt gca ata att gtc ggt ggt ttt att gta tgc tgg	1343					
175	Ala Ala Lys Thr Leu Ala Ile Ile Val Gly Gly Phe Ile Val Cys Trp						
176		435 440 445					
178	ttt ccc ttt ttc aca atg tac gta ata aga gca ttt tgt cca gac tgc	1391					
179	Phe Pro Phe Phe Thr Met Tyr Val Ile Arg Ala Phe Cys Pro Asp Cys						
180		450 455 460					
182	att cat cct gtt ctc ttc tcg gtt cta ttc tgg ctc ggc tac tgc aat	1439					
183	Ile His Pro Val Leu Phe Ser Val Leu Phe Trp Leu Gly Tyr Cys Asn						
184		465 470 475					
186	tct gcc atc aat ccg ctg att tat gca ctt ttt agc aaa gat ttc aga	1487					
187	Ser Ala Ile Asn Pro Leu Ile Tyr Ala Leu Phe Ser Lys Asp Phe Arg						
188	480 485 490 495						
190	tac gcc ttc aag cgc atc att tgc aga tac tgc ttt tgt tgc ggt aat	1535					
191	Tyr Ala Phe Lys Arg Ile Ile Cys Arg Tyr Cys Phe Cys Cys Gly Asn						
192		500 505 510					
194	cgt acc gag gcc cag cac agc ggt gga gct ggt ggt tct aga aga ggg	1583					
195	Arg Thr Glu Ala Gln His Ser Gly Gly Ala Gly Gly Ser Arg Arg Gly						
196		515 520 525					

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198 tcc gat gga tct caa atg aaa act aat ttt agg ttt aat acc agt ttt      1631
199 Ser Asp Gly Ser Gln Met Lys Thr Asn Phe Arg Phe Asn Thr Ser Phe
200      530      535      540
202 aat acc aaa aac tgc gtt cgt caa gat agt gat aat gat gtc aca aga      1679
203 Asn Thr Lys Asn Cys Val Arg Gln Asp Ser Asp Asn Asp Val Thr Arg
204      545      550      555
206 tgacccgcag ctaatgtggg attgcagagt cgagtttgaa aaaagtctag tctcaaaatc      1739
208 tgtgcaatct tgtgaattaa aaggagttaa taaagacaat cgtagagtgc cgtaaaaata      1799
210 ttttcatata atgaaaataa atcgtgaata tatcaaaaat aaattgtata agattgcatg      1859
212 taaattttaca gaaaattctt ccaaagtttt atcaatgttg gattatataa aatatgtcat      1919
214 gtaagtttta ttgagcaagc atttcaattt attgcctaaa tacaagtttt gttttcaata      1979
216 taaaatataa aatataaaaa ctgatgtaaa tagatgaaaa aataaattgt tatatttgaa      2039
218 taactaaaaa aaaaaaaaaa aa      2061
221 <210> SEQ ID NO: 4
222 <211> LENGTH: 559
223 <212> TYPE: PRT
224 <213> ORGANISM: Ctenocephalides felis
226 <220> FEATURE:
227 <221> NAME/KEY: misc_feature
228 <222> LOCATION: (192)..(192)
229 <223> OTHER INFORMATION: The 'Xaa' at location 192 stands for Ala, or Thr.
231 <220> FEATURE:
232 <221> NAME/KEY: misc_feature
233 <222> LOCATION: (193)..(193)
234 <223> OTHER INFORMATION: The 'Xaa' at location 193 stands for Asn, or Tyr.
236 <400> SEQUENCE: 4
238 Arg Tyr Val Ala Val Thr Arg Pro Val Ala Tyr Pro Ser Ile Met Ser
239 1      5      10      15
242 Thr Lys Arg Ala Lys Gly Leu Ile Ala Gly Leu Trp Val Leu Ser Phe
243      20      25      30
246 Val Ile Cys Phe Pro Pro Leu Val Gly Trp Lys Asp Lys Lys Glu Ser
247      35      40      45
250 Glu Asp Leu Ile Asp Ile Ser Ser Cys Pro Trp Thr Cys Glu Leu Thr
251      50      55      60
254 Asn Asp Ala Gly Tyr Val Val Tyr Ser Ala Leu Gly Ser Phe Tyr Ile
255 65      70      75      80
258 Pro Met Phe Val Met Leu Phe Phe Tyr Trp Arg Ile Tyr Arg Ala Ala
259      85      90      95
262 Val Arg Thr Thr Arg Ala Ile Asn Gln Gly Phe Arg Thr Thr Lys Gly
263      100      105      110
266 Ser Arg Gly Ile Gly Arg Phe Asp Glu Gln Arg Leu Thr Leu Arg Ile
267      115      120      125
270 His Arg Gly Arg Gly Gly Ser Glu Asn Arg Arg Cys His His His Ser
271      130      135      140
274 Ser Ile Lys Ser Asn Ala Ser Gly Arg Met Ser Thr Ser Thr Ser Met
275 145      150      155      160
278 Arg Asn Cys Ser Pro Gln His Ser Ser Pro Arg Ser Ala Ser Thr Ser
279      165      170      175
W--> 282 Leu Gly Ser Thr His Glu Ser Pro Glu Lys Ser Ser Ile Ser Arg Xaa

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283          180          185          190
286 Xaa Thr Trp Val Leu His His Ala Thr Asn Asn Ser Asn Ser Gly Ala
287          195          200          205
290 Cys Asn Gln Val Val Ile Ala Asn Asn Thr Ser Gln Ser Ala Pro Asn
291          210          215          220
294 Asn Asn Gln Leu Asn Ser Thr Gln Pro Glu Val Thr Val Thr Lys Ser
295 225          230          235          240
298 Ser Arg Arg Ser Ser Lys Ser Tyr Lys Ser Phe Lys Lys Glu Arg Val
299          245          250          255
302 Gln Ile Ser Val Gln Tyr Pro Ser Ala Glu Arg Leu Asp Glu Leu Glu
303          260          265          270
306 Gly Glu Leu Glu Gly Asp Ala Thr Asn Asn Met Tyr Thr Val His Tyr
307          275          280          285
310 Ser Val Ser Asn Gly Asn Ser Leu Ser Asn His Ser Leu Met Pro Glu
311          290          295          300
314 Gln Gln Ile Val Asp Ser Ser Ser Gln Gln Gln Thr Ile Arg Ala Thr
315 305          310          315          320
318 Thr Thr Ile Asn Gly Asp Gln Gln Leu Asn Ser Gly Ser Ile Tyr Arg
319          325          330          335
322 Pro Gln Asp Asn His His Leu Arg Val Thr Ser Gln Arg Leu Ala Pro
323          340          345          350
326 Ser Pro Thr Leu Ser Lys Gly Met His Arg Arg Ser Ser Ser Cys Asp
327          355          360          365
330 Ser Arg Asp Leu Ala Gly Phe Gln Leu Cys Glu Ser Ser Ser Pro Ser
331          370          375          380
334 Pro Thr Arg Arg Ile Met Ser Gly Ser Leu Tyr Arg Asp Asp Ser Glu
335 385          390          395          400
338 Leu Gly Ser Thr Ser Lys Leu Gln Gln Gln Asn Arg Lys Met Gly Lys
339          405          410          415
342 Arg Asn Ile Lys Ala Gln Val Lys Arg Phe Arg Met Glu Thr Lys Ala
343          420          425          430
346 Ala Lys Thr Leu Ala Ile Ile Val Gly Gly Phe Ile Val Cys Trp Phe
347          435          440          445
350 Pro Phe Phe Thr Met Tyr Val Ile Arg Ala Phe Cys Pro Asp Cys Ile
351          450          455          460
354 His Pro Val Leu Phe Ser Val Leu Phe Trp Leu Gly Tyr Cys Asn Ser
355 465          470          475          480
358 Ala Ile Asn Pro Leu Ile Tyr Ala Leu Phe Ser Lys Asp Phe Arg Tyr
359          485          490          495
362 Ala Phe Lys Arg Ile Ile Cys Arg Tyr Cys Phe Cys Cys Gly Asn Arg
363          500          505          510
366 Thr Glu Ala Gln His Ser Gly Gly Ala Gly Gly Ser Arg Arg Gly Ser
367          515          520          525
370 Asp Gly Ser Gln Met Lys Thr Asn Phe Arg Phe Asn Thr Ser Phe Asn
371          530          535          540
374 Thr Lys Asn Cys Val Arg Gln Asp Ser Asp Asn Asp Val Thr Arg
375 545          550          555
378 <210> SEQ ID NO: 5
379 <211> LENGTH: 2061

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/521,162

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Input Set : A:\FC-11-PCT.ST25.txt
Output Set: N:\CRF4\01252005\J521162.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 192,193
Seq#:4; Xaa Pos. 192,193
Seq#:14; N Pos. 3,9
Seq#:15; N Pos. 4,16
Seq#:33; N Pos. 8
Seq#:33; Xaa Pos. 2
Seq#:34; Xaa Pos. 2
Seq#:35; N Pos. 492

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,42,43,44,45,46,47,48,49
Seq#:50

VERIFICATION SUMMARY

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Input Set : A:\FC-11-PCT.ST25.txt

Output Set: N:\CRF4\01252005\J521162.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:623
L:282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:176
M:341 Repeated in SeqNo=4
L:1249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:1272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:1514 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
M:341 Repeated in SeqNo=33
L:1559 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0
L:1611 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:480